

## Chapter 4 - Evolutionary forces at work in fish populations

### QUESTIONS ASKED

- How do escapees from aquaculture affect genetically salmon populations in rivers?
- What are the time-scales of change in the gene pool of fish?
- Can we eradicate undesirable traits from fish stocks?
- Are small populations more or less affected by immigration?
- What genetic diversity can we expect from large stocks in the sea?
- How much, and how to avoid inbreeding in broodstocks used in fish farming?

### BACKGROUND INFORMATION

- Compendium: Santos (2015a)
- Wikipedia: [Population genetics](#)
- YouTube, by Kurz Gezagt: [How evolution works](#)



### COVERAGE

- Mutation (one-way)
- Migration (from mainland to lake)
- Fitness and selection
- Population bottlenecks
- Genetic drift

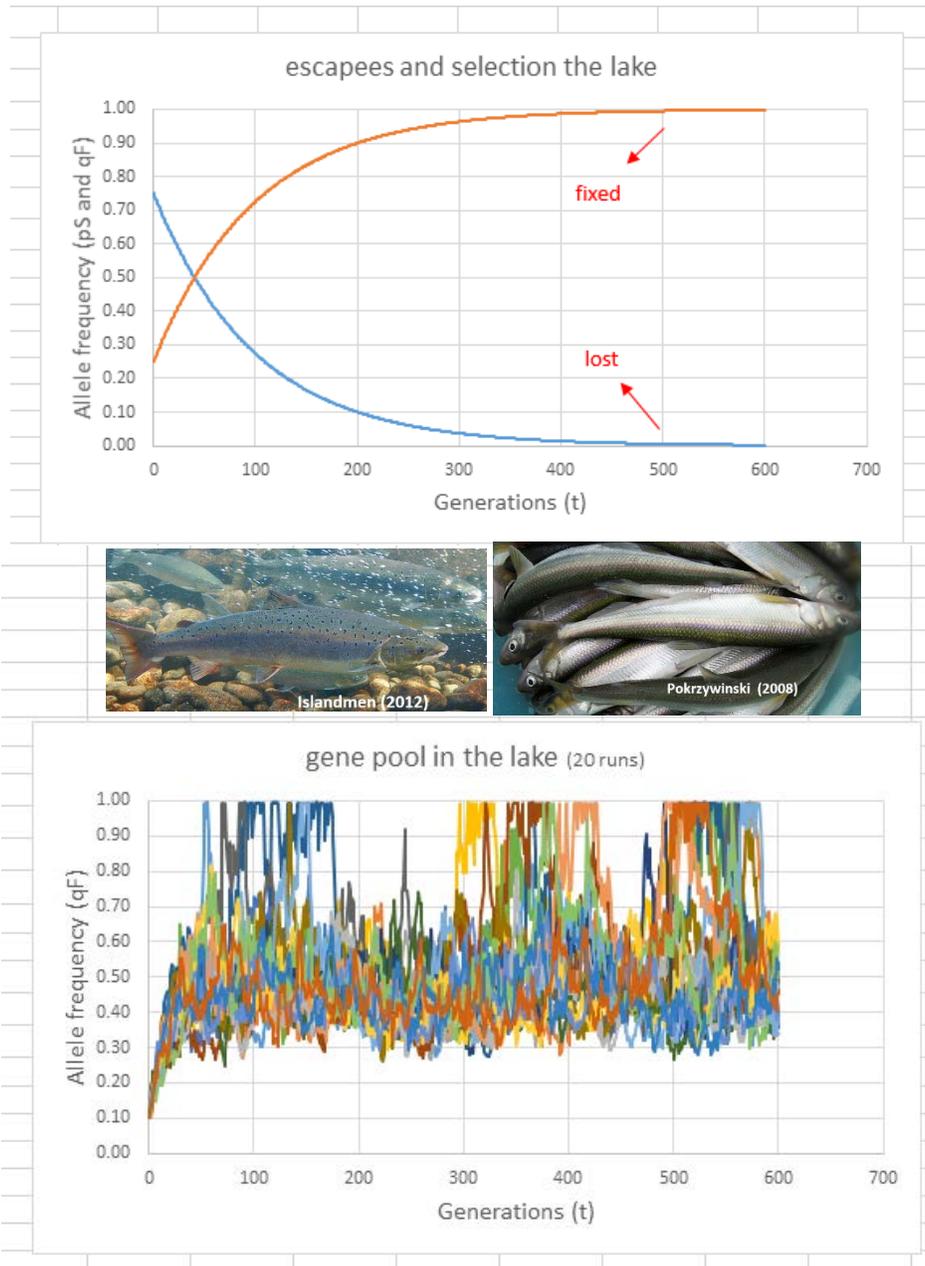
## INSPIRATION AND SOFTWARE

Originally, part of this class was performed using the software p14 and p14b developed by Jarle Mork, at NTNU in Trondheim, in the early 1990s. It is difficult to run that software in today's operative systems. I adapted those versions to Excel. One of the programmes includes deterministic models and the other is stochastic, to account for the effects of stock size and drift. The last software comes, thus, available as a macro version of an Excel workbook. It normally requires special enabling by the user.

- [Ch4a Population genetics migration selection deterministic JdS.xlsx](#)
- [Ch4b Population genetics drift stochastic macro JdS.xlsm](#)



## SNAPSHOTS



## THE ASSIGNMENT

### ***Selection, immigration and genetic drift.***

The Inputs are:

- (mean) population size; (all individual reproduce; panmixy)
- variability of the mean population size, expressed as the SD (individuals) of the mean. It is used to simulate bottlenecks.
- gene frequency  $q_F$  of the original population (and of immigrating individuals, if required).
- Number of immigrants per generation, if required
- Relative fitness of the three genotypes
- number of iterations is fixed
- all selection forces are optional, but can also be used together.

The output are line graphs showing the change in the mean fitness and gene frequencies with generations of the lake population.

***There was once a small landlocked population of (diploid !!) salmon...***

- 1- In a small, landlocked (isolated) population of salmon (100 fish) ten of the salmon turn out to have one mutated allele at the S locus, which was previously fixed (only SS fish). But this new mutation (F) does not seem to reduce their capacity to survive and reproduce. How many salmon are expected to have acquired the mutated gene after 100 generations, excluding the effects of genetic drift?

(Note: 100 fish x 2 alleles = 200 alleles; of these 10 are mutations, and this gives  $q_{mut} = q_F = 10/200 = 0.05$ )

- 2- The same, but now with genetic drift. What do you conclude?
- 3- The same as 2), but now consider that this population varies considerably in size from generation to generation, with an estimated standard deviation corresponding to 30% of the mean population size. What do you conclude?

4- A new problem with a landlocked population. The lake owner, Mr. Killa, decides to get rid of the fish that shown the “FF syndrome”, because they are really ugly. “It may take me some years...but these f...f... will disappear!” He kills every parr (immature salmon) there is affected with this FF-syndrome. As the name says, the FF-syndrome is only visible in the homozygous state, and the fish that possess the F gene are as capable as any other. Besides, even if they are really ugly there is no uncommon sexual selection for them. On average, there are 4 FF fish for the 100 fish in the lake, and no genetic drift, nor bottlenecks in the population. How many years will have Mr. Killa to wait to get a lake clean of the F gene, taking into account that the reproductive age of these fish is 6 years.?

(Note: according to the Hardy-Weinberg law the phenotype FF corresponds to the genotype frequency  $q^2$ . If  $FF=4$  then  $q_F=0.2$ . The selection pressure on this homozygote is 1, and its fitness is thereby 0. This problem resembles the eugenics dilemma.)

5- The fish that have a new mutation F ( $q_F=0.05$ ) in the homozygote state have a slightly higher (5%) *relative fitness* than the heterozygotes, and 10% higher *relative fitness* than the SS homozygotes. The population is *panmictic*,  $N=100$ , and there is genetic drift and bottlenecks (20% SD of the mean  $N$ ). What do you conclude?

**...they built a channel down the lake, and now the farmed (diploid) salmon are invading it....**

6- Every generation one farmed salmon manages to pass the traps in the channel that leads to the lake. The original gene frequency in the lake is  $q_F=0.8$  but the invading salmon does not have this allele F. How will the population look like many years from now with regard to this locus? (No genetic drift, nor bottlenecks in the population, and all genotypes have similar fitness.)

7- The thing is getting out of control! Every generation 20 farmed salmon (20% of the population !!!) enter and reproduce in the lake. Invaders have a strange mating behaviour and only have a 50% chance of reproducing in relation to the wild variant. The hybrids only perform 25% worse than the wild salmon. How many years until the wild genotype is decimated? (Same parameters as in 6).)

(Note: here sexual selection is the type of selection acting on the fitness of the fish.)

8- The size of the local spawning population has considerably varied in the last 10 years: 100, 130, 150, 100, 80, 40, 100, 40, 100, 120. Calculate the effective population size ( $N_e$ ) of the reproductive population. (Hint: calculate the

arithmetic, the geometric and the harmonic means and backcalculated standard deviations. It is the harmonic mean that gives the  $N_e$ .

Formulas:

arithmetic mean = " $N_e$ " =  $\frac{1}{t} * \sum_1^t N_t$ ; geometric mean = " $N_e$ " =  $anti \ln \left( \frac{1}{t} * \sum_1^t \ln N_t \right)$

harmonic mean =  $\frac{1}{N_e} = \frac{1}{t} * \sum_1^t \frac{1}{N_t}$ ; Remember that we know the TOTAL population size

when you compute the standard deviation.

**... meanwhile, down the river, in the hatchery...**

- 8- The hatchery has kept 600 spawners, in a sex ratio of 1:1 as in nature. This programme has already been very expensive. Last year the hatchery decided to keep only 20 males in addition to the 300 females. What is the  $N_e$ ?

Formulas

When the two sexes do not contribute equally to the genes in the next generation, the effective number is twice the harmonic mean of the numbers of the two sexes, and that is approximately:

$N_e = \frac{4 * N_f * N_m}{N_f + N_m}$ . This requires that the probability of reproductive success is equal for all

individuals (e.g. do not pool the milk and eggs in the buckets).

- 9- New rules state that it is necessary to avoid rates of inbreeding ( $\Delta F$ ) at levels higher than 1% per generation. Is the present spawning population structure satisfactory?

Formula:  $\Delta F = \frac{1}{2N_e}$

**...out in the sea there is a large population of diploid capelin....**

- 11- Repeat problems 3, 5 and 6 with a population size of 30 million.  
12- Repeat problem 5 with capelin, but this time use a SD of 35% of the population size to simulate bottlenecks. Did any "extinction" occur? Why?

Note: the problem here lies on the statistics, not in the population genetics: if sd is larger than 30% of the mean, then according to the normal distribution mean - 3sd is less than 0, and the population vanishes irrespective of the gene frequency.